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DEFINITION				
Sequence 7086 from Patent Ep1108790.				
ACCESSION				
AX127150				
VERSION				
AX127150.1				
KEYWORDS				
AX127150.1				
GI:114041138				
SOURCE				
ORGANISM				
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Corynebacterium glutamicum.				
Corynebacteria; Firmicutes; Actinobacteria; Actinobacteriidae;				
Actinomycetales; Corynebacteriinae; Corynebacteriaceae;				
Corynebacterium.				
1 (bases 1 to 349980)				
REFERENCE				
AUTHORS				
Nakagawa, S., Mizouchi, H., Ando, S., Hayashi, M., Ochiai, K.,				
Yokoi, H., Tateishi, N., Senoh, A., Ikeda, M. and Ozaki, A.				
TITLE				
Novel polynucleotides				
JOURNAL				
Patent: EP 1108790-A 7066 20-JUN-2001;				
KIOWA HAKKO KOGYO CO., LTD. (JP)				
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source				
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Location/Qualifiers				

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 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1581; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 DEFINITION Sequence 2362 from Patent EP1108790.
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 VERSION AX122446.1 GI:14039691
 KEYWORDS
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 ORGANISM
 Corynebacterium glutamicum.
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 Bacteria: Firmicutes; Actinobacteria; Actinobacteriales;
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 Corynebacterium.
 1 (bases 1 to 1458)
 REFERENCES
 Nakagawa, S., Mizoguchi, H., Ando, S., Hayashi, M., Ochiai, K.,
 Yokoi, H., Tateishi, N., Senoh, A., Ikeda, M. and, Ozaki, A.
 Novel polynucleotides
 Patent: EP 1108790-A 2362 20-JUN-2001;
 JOURNAL
 KYOWA HAKKO KOGYO CO., LTD. (JP)
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 Best Local Similarity 100.0%; Pred No. 0;
 Matches 1458; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 3

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 AB015023.1 GI:3868934
 VERSION
 KEYWORDS
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 ORGANISM
 Corynebacterium glutamicum DNA.
 Bacteria; Firmicutes; Actinobacteria; Actinobacteriales; Corynebacteriales; Corynebacteriaceae; Corynebacterium.

REFERENCE
 1 (bases 1 to 2291)
 Wachi, M.
 Direct Submission
 Submitted (27-MAY-1998) to the DDBJ/EMBL/GenBank databases. Masaki Wachi, Tokyo, Institute of Technology, Department of Bioengineering; 4259 Nagatsuta Midori-Ku, Yokohama, Kanagawa 226-8501, Japan (E-mail: mwachi@bio.itech.ac.jp, Tel: 81-45-924-5770, Fax: 81-45-924-5820)

2 (sites)
 Wachi, M., Miyazawa, C.D., Terada, H. and Nagai, K.
 A murc gene from coryneform bacteria
 JOURNAL
 Appl. Microbiol. Biotechnol. (1998) In press
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	ACCESSION	E28467		
	VERSION	E28467.1 GI:13018359		
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	ORGANISM	Corynebacterium glutamicum.		
		Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;		
		Actinomycetales; Corynebacterineae; Corynebacteriaceae;		
		Corynebacterium.		
	REFERENCE	1 (bases 1 to 1458)		

JOURNAL Unpublished
REFERENCE 2 (bases 1 to 4622)
AUTHORS Gil, J. A.
TITLE Direct Submission
JOURNAL Submitted (17-MAY-1999) Gil J. A., Microbiology, University of Leon,
Campus de Vegazana s/n, 24071 Leon, SPAIN
Location/Qualifiers

102A

FEATURES

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AGSGMDGVGIPRAVLSGARDSEADARPDGKDRDROFTITVSGSGSISIKKA
VEGADIDLVGAEFOVLAHVKKNELPAKRGHPPTDDMAATYADLVIVRSKM
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3147. 4607
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/db_xref="GI:6723459"

gene

CDS

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GATVALGARGLETTVPDREGFELHLEPVYPRKNDLKLPLFVNAALGQAKA
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AGSGMDGVGIPRAVLSGARDSEADARPDGKDRDROFTITVSGSGSISIKKA
VEGADIDLVGAEFOVLAHVKKNELPAKRGHPPTDDMAATYADLVIVRSKM
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/transl_table=11
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/protein_id="CAB6325.1"
/db_xref="GI:6723459"

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DAKDSRTLLPLPAGATIAVGAENLEISGLPVTYVTSRAIPONPELVAREEG
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TAAHGTGEFTIADSDASLARIKPAVAVTNVPEPHLFFETPEATYQVDFDAG
RTTPNGKLVLNDPAAELGERSVKRGKRTGYOTRAVOAHEVPAATVDDSOV
AGTBRATINIDGOEVSIIQIPDHWLGAALAGLVGDDVDKLEISDFSGVR
RRFEFGAIEGGKFNCAIYDDVAHHPTETVTLRRCATRYAKAGKRVIAVQPHLY
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BASE COUNT 989 a 1254 c 1317 g 1062 t
ORIGIN

Query Match 60.2%; Score 951; DB 1; Length 4622;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1201; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 1 gcaagtaacgcctccacagtgatctgacacatctgacacatcaatgccaacac 60
DB 3047 GCAGTAAACCCCTCCACGCTGATTCACACATGATTCCTCAATCAATGCCAACAC 3106
QY 61 aactaaacgaacacagctcaacgaagaatagtttaagtgacacacacacactgga 120
DB 3107 AACTAAACGACACGCTCAACGCAAGAAATGTTAAAGTGACCACTCAGACTTGA 3166
QY 121 ttctgcacaagatattgacatctccgcgtccacatcgcgattgagcgagcggaat 180
DB 3167 TTCGCAACAGATATGATCTCTCCGCGTCCACCTATGCGRTTGGCGAGCCGGAAT 3226
QY 181 gtctgagcgttgcgcgaatccctgcttgcgcgtaagaacatcgtgtccgatgca 240
DB 3227 GTCTGCGGTTGCCGAAATCTGCTGCCGCGGTAAACAGTACGTGTTCCGAGGCCAA 3286
QY 241 agatcccgacaccttctccacatccgcgcgttgagagcaccatcgagtgagacagc 300
DB 3287 AGATTCCCGACCTTCTCCATCCGCGCGGTGAGGACCACTGAGTGAGGACACG 3346
QY 301 tgcggaacacactgagcttccgcggaactccacacgttggtgacactcttgcgcg 360
DB 3347 TCGGGAACACTTGACCTTCCGCGAATCTCCACCGCTGTGTGATCCTCTTTGCGCG 3406
QY 361 catccgcaagacacacgcgaactgttctgacgctgaaagagacatccggtatctg 420
DB 3407 CATCCCGCAAGAACACCGCAACTGTTCGCGACGAGGAAGGCAATCCGTTATTGC 3466
QY 421 tgcgtccgacatctgttgaggaattgctgaaagagctccacacaggtctgagcgtac 480
DB 3467 TCGCTCGAATCTGTGGGGAATTCCTGGAAGGCTCCACCAAGTCTTATGCGGGTAC 3526
QY 481 ccacgtaagaacctccacacactatgctgtgtagctatgacgaagcgggcatgga 540
DB 3527 CCACGGTAAGACCTCCACACCTCTATGCTGTGTGATGACAGCGAGCGGCAATGA 3586
QY 541 tccaagcttgcctatcgcgcgacgacgacgaagcgtgacacacacacacacacac 600
DB 3587 TCCAAGCTTTGCTATCGAGGGGAGACAGCTCAACAAAGCTGGCAGCAACGACGAGAC 3646
QY 601 tgtgtgaggtcttattcgtctgaaagcagatgaaatctgacgacatcgtcgtcgctacacgc 660
DB 3647 TGGTGAAGTCTTATCGCTGAAGCAGATGAATGAGAGCATGCTGCTGCTGCTAACAACC 3706
QY 661 aaatgttcagtgagtcacaaatgtgaaacacgaacacacacacacacacacacac 720
DB 3707 AAATGTTCAGTGTGACCAATGTGAACCAAGACACCTGACTTCTTAAACCCCTGA 3766
QY 721 agctctactccaagtggttcgacagatttcgacagacacacacacacacacacacac 780
DB 3767 AGCTTACTTCCAGATGTTGAGAGATTTCGAGGAGCAGATCCGACGAGGACGAGCTGT 3826
QY 781 tgtgtgcctgaagacatccctcacgacgagcgttggtgagaggtctgtccgcaaggtat 840
DB 3827 TGTGTGCTGAAGCATCTCTACGACGAGCGAGCTGGGAGAGAGTGTGTCCGAGAGGAT 3886

OY	841	caagactgttcttaacgtagtcacgcctcaccgaagaacacctgagttccaggcat	900
Db	3887	CAGACTGTGTTACGGTACCGCTGAGCAGATACGACACCCTTGAGCTTCAGGCAT	3946
OY	901	ggtctccatctgttgattccccaaagtgtgtcgcaagaagcccggccaccataacatcga	960
Db	3947	GGTCTCCGCTGTTGATTGCCAAATGTTCTCCAGAAAGGCAACCGGCCCATCAATCAATCA	4006
OY	961	tggacagagaagatcttgtattcttcctaacccttggtgatcacatigtactaacggttc	1020
Db	4007	TGCACAGGAAGTACTGTGATTTCTTAATCCCTGCTGGATCACATGTAATCAACGGTGC	4066
OY	1021	agccgccctgttcggccggatctctgtgtgtgtggagagcttgacaacatgtttgaagcgt	1080
Db	4067	AGCCGCCCTGCTGGCCGGATACCTGTTGGGTGGGAGCTGATAAAGCTTTGTAAGCTT	4126
OY	1081	gtcggatttctccggcgtgtgcagccgcctttgattccacggtgctactcgaggcggcaa	1140
Db	4127	GTCGGATTTCTCCGGCTGTGGACGCCGCTTGAGTCCACGGAGCTATGAGAGGGCGCAA	4186
OY	1141	attaatgtgagctctgatttatgtatgtatgaacacacacccaacggaagtactgcagt	1200
Db	4187	ATTATATGGCGCTGCTATTATGATGATTAACCAACACCAACCAAGAGTAATGCGNGT	4246
OY	1201	gtccag 1206	
Db	4247	GCTCA 4252	
RESULT	6		
LOCUS	AB003132	4116 bp DNA	BCT 04-AUG-1997
DEFINITION	Corynebacterium glutamicum gene for murC, ftsQ, complete cds		
VERSION	AB003132		
KEYWORDS	FtsZ; FtsQ; MurC.		
SOURCE	Corynebacterium glutamicum		
ORGANISM	Corynebacterium glutamicum Bacteria; Firmicutes; Actinobacteria; Actinomycetales; Corynebacteriaceae; Corynebacteriales;		
REFERENCE	1 (bases 1 to 4116)		
AUTHORS	Kobayashi,M.		
TITLE	Direct Submission		
JOURNAL	Submitted (15-APR-1997) to the DDBJ/EMBL/GenBank databases. Miki Kobayashi, Mitsubishi Chemical Corp., Tsukuba Research Center; Ami E-mail: 3709293@cc.m.kagaku.co.jp, Tel:0298-87-1011, Fax:0298-87-3259)		
REFERENCE	2 (sites)		
AUTHORS	Kobayashi,M., Asai,Y., Hatakeyama,K., Kijima,N., Wachi,M., Negai,K. and Yokawa,H.		
TITLE	Cloning, sequencing, and characterization of the ftsQ gene from Coryneform bacteria.		
JOURNAL	Biochem Biophys Res Commun. 236 (2):383-388(1997)		
MEDLINE	97382442		
FEATURES	Location/Qualifiers		
source	1..4116		
gene	/organism="Corynebacterium glutamicum"		
CDs	/db_xref="taxon:1718"		
gene	1..273		
CDs	/gene="murC"		
gene	<1..273		
CDs	/gene="murC"		
gene	/codon_start=1		
CDs	/transl_table=11		
gene	/product="MurC"		
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gene	/db_xref="gi:2308990"		
CDs	/translation="EPOKEFALSLADAAYVLELYGARBPVDGVSELTIDANTITIVYVEHPMSAVPRRIAEIENGRNDVLTMGASVTMLAPEILDQLNN"		
gene	301..969		
CDs	/gene="ftsQ"		

301..969
/gene="fts0"
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/transl_table=1
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/translation="MKRVIAIVGVVVVLAIIIGVAMEVPIIKVGNIEVGAIRTD
PDVLESGVIGENLEFNKVDATAAGNIIEIEMKSTVVRALPSTIYTELIERPAV
FIRAGDHVITDEKEIIGTTPVGVTSVCSADGENSEVLPVIVIAIAIDAOQADH
TESIVGVEAPDQFDILKMHNDGREIYMGSENHNHDKAVAMSTVILKRDGQRMNLS
VTVR"

1220..2536
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1220..2536
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OALMFSDAVKLDIGREKATGLGAGNPEVGSASEYKHNEIETIKGADVFTAGEE
GGAGGAGAPVYVGRGKATKMGALITGVYTPPEFEGERTROAEETIAEKVCTILIV
IPNDRLLEIAGANLSIMEFRAADVPLHNGVGTNLITPCTINDPADVRSVSEAG
SALMGCSRGDNRRVVSATQCALINSPLRTMDATGYLLSPFGSGLDEMEVNAAS
MKREDEDEVNLTFTIITDNLGDEVYRVITGDARKSAAENRRAGTIPAPAAAE
VQ00YQVPTNATLPEKESIEFGAREENPYLSRAGARRIETRSGGGLPTTGNDR
DYRDDRRRDRHDERDRDRSYDRDRDRDRDRGDDLPSTFLO"

2564..3304
/note="hypothetical protein similar to yfiH"
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/db_xref="GI:2308993"
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SNRRADITGSLSPKYYVMEQIHSTYVVIDEAPAGCAVEATDLYTTONGALAAV
LVNDCVPLVSTDAGVYIAAVHNGRGAANGVIAATIKMEIGANPSITHLMKAAAE
SGAKVYEPAAARDEAKLEPGSLARTKCTGTGLDIRAGLLROMLSGVGMIDSPRCT
IEDEDFSYRRCTGTGGAGVWVLPKEA"

3345..4010
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/db_xref="GI:2308994"
/translation="NQRIDATLNEHNPRESSVRLPLVYTFHVEDIKILQLEGLTAV
GNERDEARAKALEPMDHMTIGQIOSKKAASIAKSAVHVSDEKTAEMALGVGA
LAEREDSDIDELPCFTIOLSDPSRGSTPLISQVTLALDCISDTTHLEFEDMLVPP
PLWDPKAFSAQRVDVLSGLEHEDRSLFESAGMSGDLVAAIKKGSTIVRGYTHLGNR
LVA"

BASE COUNT 1009 a 1106 c 1148 g 853 t

ORIGIN

Query Match 14 98: Score 236; DB 1; Length 4116;
Best Local Similarity 100.0%; Pred. No. 5.7e-119; Indels 0; Gaps 0;
Matches 236; Conservative 0; Mismatches 0

Db 1346 gagattacgagagcgcgagacaacccggtgagatgagcgctgctcctcggaatacatcaccgat 1405
Db 58 GAGATTTCACGAGAGCGCGGACACACCGGTGATGCGCTGCTCGGAATCATCATCCGAT 117
GAGATTTCACGAGAGCGCGGACACACCGGTGATGCGCTGCTCGGAATCATCATCCGAT 117
Db 1406 gcatgacattccagctggtgtctgagacctaatctctcctcaatccacgaagcattgca 1465
gcatgacattccagctggtgtctgagacctaatctctcctcaatccacgaagcattgca 1465
Db 118 GCGATGACCATTCACAGTGGTGATCGACACTAATTCTCTGCGAGTCCGAGAACGATTGCA 177
GCGATGACCATTCACAGTGGTGATCGACACTAATTCTCTGCGAGTCCGAGAACGATTGCA 177
GCGATGACCATTCACAGTGGTGATCGACACTAATTCTCTGCGAGTCCGAGAACGATTGCA 177
Db 1466 gaatacgaagaacctaatgacatctgtctcaccatgggtgagcggtcttcgtaacatgctt 1525
gaatacgaagaacctaatgacatctgtctcaccatgggtgagcggtcttcgtaacatgctt 1525
Db 178 GAAATGCGAGGAGCTAAATGACATCGTCTCACACATGGGTCAGAGTCCGTGATCATCTT 237
GAAATGCGAGGAGCTAAATGACATCGTCTCACACATGGGTCAGAGTCCGTGATCATCTT 237
GAAATGCGAGGAGCTAAATGACATCGTCTCACACATGGGTCAGAGTCCGTGATCATCTT 237
Db 1526 gctccaagaatcctcgatcagctgcaaaaaaatattaggaagctaaagtgaacaagcag 1581
gctccaagaatcctcgatcagctgcaaaaaaatattaggaagctaaagtgaacaagcag 1581
gctccaagaatcctcgatcagctgcaaaaaaatattaggaagctaaagtgaacaagcag 1581

Db 238 GCTCCAGAAATCTGATGATGCTGCAAAACAAATAGGACGTAGTGAACAAGCAG 293

RESULT 7
BLPFSZ 5546 bp DNA BCT 19-JAN-2000
LOCUS Brevibacterium lactofermentum murc(Partial), ftsQ, ftsZ genes and
DEFINITION ORS5, ORF6 DNA.
ACCESSION Y08964.2 GI:6723445
VERSION Y08964.2
KEYWORDS cell division protein; divb gene; division initiation protein; ftsQ gene; ftsZ gene; murc gene; putative YAK 1 protein; putative YP75 protein; UDP-N-acetylmuramate-alanine ligase.
SOURCE Corynebacterium glutamicum.
ORGANISM Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Corynebacteriaceae; Corynebacterium.
REFERENCE 1 (bases 1 to 5546)
AUTHORS Honruba, M.P., Fernandez, F.J. and Gil, J.A.
TITLE Identification, characterization, and chromosomal organization of the ftsZ gene from Brevibacterium lactofermentum
JOURNAL Mol. Gen. Genet. 259 (1), 97-104 (1998)
MEDLINE 98409265
REFERENCE 2 (bases 1 to 5546)
AUTHORS Gil, J.A.
TITLE Direct Submission
JOURNAL Submitted (21-OCT-1996) J.A. Gil, Universidad de Leon, Microbiologia, Campus de Vegazana S/N, 24071 Leon, SPAIN
REMARK Revised by [3]
AUTHORS 3 (bases 1 to 5546)
TITLE G11, J.A.
JOURNAL Direct Submission
COMMENT Submitted (24-MAY-1999) J.A. Gil, Universidad de Leon, Microbiologia, Campus de Vegazana S/N, 24071 Leon, SPAIN
FEATURES
Location/Qualifiers
1..3546
/organism="Corynebacterium glutamicum"
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/gene="murC"
CDS <1..264
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/codon_start=1
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/protein_id="CAA70156.1"
/db_xref="GI:1769959"
/db_xref="SPTREMBL:P94335"
/translation="KEFAALSLADAIVLEIYGAREPVDGVSSEIITDMATIPVY
EPNFSVAPRIAEINGPNDIVLTMGAGSYMLAPILDLQNN"
292..960
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292..960
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/note="alternative gene name divb"
/codon_start=1
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/db_xref="GI:1769960"
/db_xref="SPTREMBL:P94336"
/translation="MNRKVAIVGVVAVLVAILGVAVFVILKNGIEVGTATRD
PDQVLESGVIGENLFRVDAIAGONIYELPVRKSVYVNRALPSTIVELTEEPYV
FIRAGSDHVIDTEKEKIIIGTPVGVESGADENSIVLPVAVIAVINAKIKRODADM
TESIQVVEAPDQFDILLKMGDSREIYGSSENNHDAVAMSVILKREGRNINSSPEN
VTVR"
1211..2527
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CDS 1211..2527

Query Match 14.9% Score 236; DB 1; Length 5546;
Best Local Similarity 100.0%; Pred. No. 5.5e-119;
Matches 236; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 49 GAGATTTCAGGACGGCGGACGACACCGGTGATGCTGCTCCGGAATCATCACCAT 108

QY 1346 gagatttcagagcgcgcaaacaccggtggaatgagctgctcctggaaatcaacgcat 1405

Db 109 GCGATGACCATTCACATGCTGTGACGACACCATTAATTCCTGCAATCCCAAGCAATTGCA 168

QY 1466 gcaatgcagacctaataatgctgctccaatcctcctcagtcagtcagcaagcattgca 1465

Db 169 GAAATCGACGACCTAATGATCGTCTCACCATGAGTCCAGATTCCTGACATGCTT 228

QY 1526 gctccagaatcctgcatcagctgcaaaacattagagctgaagtgacaagcgacg 1581

BASE COUNT 1317 a 1479 c 1520 g 1230 t

ORIGIN

4118..4576
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/transl_table=11
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/protein_id="CAB66326.1"
/db_xref="GI:6723446"
/translation="MQARIDATLTNHNRRPESGVRLPYTKFHPVEDIKIIOELGVAV
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4118..4576
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/codon_start=1
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/protein_id="CAB66327.1"
/db_xref="GI:6723447"
/translation="MSMLKTKKEFGIARVEAEHEDAYNADEPRREGTAAYAPRYER
DYGVPKPAVYAPASRPAPRSYOSTIVPELHSEFDNOYIGAFRGGAVFDMSLSR
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Db 229 GCTCCGAATCTGATCAGTGCACAAACAAATGAGACGTATGACCAAGGAG 284

RESULT 8

AX122447 AX122447 1116 bp DNA PAT 11-MAY-2001
 DEFINITION Sequence 2363 from Patent EP1108790.
 ACCESSION AX122447
 VERSION AX122447.1 GI:14039694
 KEYWORDS
 SOURCE Corynebacterium glutamicum.
 ORGANISM Corynebacterium glutamicum
 Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 Actinomycetales; Corynebacteriaceae; Corynebacteriaceae;

REFERENCE

AUTHORS Nakagawa, S., Mizoguchi, H., Ando, S., Hayashi, M., Ochiai, K.,
 Yokoi, H., Tateishi, N., Senoh, A., Ikeda, M. and Ozaki, A.
 TITLE Novel polynucleotides
 JOURNAL Patent; EP 1108790-A 2363 20-JUN-2001;
 KYOKA HAKKO KOGYO CO., LTD. (JP)

FEATURES

source Location/Qualifiers
 1..1116
 /organism="Corynebacterium glutamicum"
 /db_xref="taxon:11718"
 BASE COUNT 234 a 317 c 319 g 246 t
 ORIGIN

Query Match

Best Local Similarity 100.0%; Score 63; DB 6; Length 1116;
 Matches 63; Conservative 0; Pred.No. 4.8e-23; Mismatches 0; Indels 0; Gaps 0;

QY 1 gcaggaacgcctccacggtatgacagatgattgctgcacatcatgacacac 60
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 Db 1054 GCAGGAACGCTCCACGCTGATGACAGATGATGCTGCACATCATGACCAAC 113
 QY 61 aac 63
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 Db 1114 AAC 1116

RESULT 9

AF022730 1073 bp mRNA PLN 30-OCT-1997
 LOCUS Oryza sativa glyceraldehyde-3-phosphate dehydrogenase subunit
 DEFINITION (GAPDH) mRNA, partial cds.
 ACCESSION AF022730
 VERSION AF022730.1 GI:2570494
 KEYWORDS
 SOURCE Oryza sativa.
 ORGANISM Oryza sativa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.
 1 (bases 1 to 1073)
 Lee, M.C., Kim, C.S. and Eun, M.Y.
 TITLE Isolation and characterization of glyceraldehyde-3-phosphate
 dehydrogenase from rice
 JOURNAL Unpublished
 2 (bases 1 to 1073)
 Lee, M.C., Kim, C.S. and Eun, M.Y.
 TITLE Direct Submission
 JOURNAL Submitted (04-SEP-1997) CytoGenetics, National Institute of
 Agricultural Science and Technology, RDA, Sedun-Dong, Suwon
 441-707, Korea
 FEATURES
 source Location/Qualifiers
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 /strain="Milyang 23"
 /db_xref="taxon:4530"
 /tissue_type="seed"

/dev_stage="Immature (milk stage)"
 /clone="KCDW2189"
 1..>1073
 /gene="GAPDH"
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 VSRFNAVCTNGARAPRTAKIKVAINGRGRGRLICWGRGDSPLNIPINT
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 CTNCCAPFVKILDQKFGIIRKMTTSTGDRVFDGSHRDLRRARAALNIVPTS
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 ELKASSRER"

BASE COUNT 196 a 380 c 335 g 162 t
 ORIGIN

Query Match

Best Local Similarity 100.0%; Score 21; DB 8; Length 1073;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1076 ggcctgctgcgattctccgcgc 1096
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 Db 93 GCGTTGTGCGATTCTTCGCCGC 113

RESULT 10

AC019805/6 6843 bp DNA HTG 03-JAN-2000
 LOCUS Drosophila melanogaster. *** SEQUENCING IN PROGRESS *** in ordered
 DEFINITION pieces.
 ACCESSION AC019805
 VERSION AC019805.1 GI:6665092
 KEYWORDS HTG; HTGS_PHASE2.
 SOURCE fruit fly.
 ORGANISM Drosophila melanogaster
 Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
 Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
 1 (bases 1 to 6843)
 Adams, M. and Venter, J.C.
 TITLE Direct Submission
 JOURNAL Submitted (30-DEC-1999) Celera Genomics, 45 West Gude Drive,
 Rockville, MD, USA
 COMMENT This sequence was identified as CDW:10211017 by the submitter.
 For more information on this record e-mail to fly@celera.com.
 * NOTE: This is a 'working draft' sequence.
 * This sequence will be replaced
 * by the finished sequence as soon as it is available and
 * the accession number will be preserved.
 FEATURES
 source Location/Qualifiers
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 /organism="Drosophila melanogaster"
 /db_xref="taxon:7227"

BASE COUNT 1966 a 1466 c 1449 g 1962 t
 ORIGIN

Query Match

Best Local Similarity 100.0%; Score 21; DB 2; Length 6843;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 262 actccgcgcgtggagccac 282
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 Db 5976 ACTCCGCCTGCGAGCCAC 5956

RESULT 11

AC010010

LOCUS AC010010 85875 bp DNA HTG 18-FEB-2000
 DEFINITION Drosophila melanogaster clone RPCI98-13F6, *** SEQUENCING IN
 PROGRESS ***, 53 unordered pieces.
 ACCESSION AC010010
 VERSION AC010010.3 GI:6996694
 KEYWORDS HTG, HTGS_PHASE1.
 SOURCE fruit fly.
 ORGANISM Drosophila melanogaster
 Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
 Muscomorpha; Phlebotomidae; Drosophilidae; Drosophila.
 1 (bases 1 to 85875)
 Munz, D.M., Adams, C., Bailey, M., Barberia, J., Blankenburg, K.,
 Bodota, B., Bouck, J., Bowle, S., Brooks, A., Buhay, C., Bunc, C.,
 Burkett, C., Burrows, J., Carter, M., Chacko, J., Chen, Z., Cox, C.,
 David, R., Delgado, O., Deshazo, D., Ding, Y., Domah-Rashid, N.,
 Dugan-Rocha, S., Durbin, K.J., Fernandez, C., Ferraguto, D.,
 Forcum-Tansey, J., Frantz, P., Ganesh, R., Gorrell, J.H., Gorrell, L.L.,
 Guevara, M., Harris, K., Hernandez, J., Hodgson, A., Hogue, M.,
 Holloway, C., Hosak, R., Jackson, L.E., Jackson, L., Jia, Y., Jones, M.,
 Kelly, S., Kondajewski, N., Kong, Y., Kovar, C., Leal, B., Li, Z.,
 Licherage, O., Liu, J., Liu, W., Logan, O., Lozano, R.J., Lu, J.,
 Martin, R., Martin, R., Martinez, C., McLeod, M.P., Mei, G., Morgan, M.,
 Morris, S., Nash, S., Nelson, A., Nguyen, R., Nguyen, N., Nguyen, S.,
 Owsal, G., Parish, B., Paxton, S., Payton, B., Perez, L., Pu, L.L.,
 Quiles, M., Reiter, D., Rives, M., Samuel, S., Say, J., Scherer, S.,
 Shah, E., Shen, H., Simon, M., Sparks, A., Stamps, R., Sugrue, R.,
 Taber, P., Taylor, T., Vasquez, L., Vinson, R., Vo, Q., Wadham, M.,
 Wellington, S., Weinstein, G., Weinstein, I.R., Williamson, A.,
 Worley, K., Wren, J., Wrenford, G., Yu, W., Zhou, X., Nelson, D. and
 Gibbs, R.
 Direct Submission
 Title
 JOURNAL
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT
 Submitted (11-SEP-1999) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
 On Feb 18, 2000 this sequence version replaced gi:5881484.
 ----- Genome Center
 Center: Baylor College of Medicine
 Center code: BCM
 Web site: http://www.hgsc.bcm.tmc.edu/
 Contact: hgsc-help@bcm.tmc.edu
 ----- Project Information
 Center project name: RPCI98-13F6
 Center clone name: RPCI98-13F6
 ----- Summary Statistics
 Sequencing vector: M13; L08821
 Chemistry: Dye-terminator Big Dye; 68% of reads
 Assembly program: Phrap; version 0.980611
 Consensus quality: 41466 bases at least Q40
 Consensus quality: 57245 bases at least Q30
 Consensus quality: 64739 bases at least Q20
 Estimated insert size: 75108; sum-of-coverage estimation
 Quality coverage: 0.8x in Q20 bases; sum-of-coverage estimation

 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 53 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.
 * 1 1256: contig of 1256 bp in length
 * 1257 1276: gap of unknown length
 * 1277 2355: contig of 1079 bp in length
 * 2356 2375: gap of unknown length
 * 2376 3452: contig of 1077 bp in length
 * 3453 3472: gap of unknown length

3473 4275: contig of 803 bp in length
 4276 4295: gap of unknown length
 4296 5562: contig of 1267 bp in length
 5563 5582: gap of unknown length
 5583 6777: contig of 1195 bp in length
 6778 6797: gap of unknown length
 6798 8061: contig of 1264 bp in length
 8062 8081: gap of unknown length
 8082 9053: contig of 972 bp in length
 9054 9074: gap of unknown length
 9074 9934: contig of 861 bp in length
 9934 9954: gap of unknown length
 9955 10765: contig of 812 bp in length
 10766 10786: gap of unknown length
 10787 11616: contig of 830 bp in length
 11617 11636: gap of unknown length
 11637 12464: contig of 828 bp in length
 12465 12484: gap of unknown length
 12485 13645: contig of 1161 bp in length
 13646 13665: gap of unknown length
 13666 14489: contig of 824 bp in length
 14490 14510: gap of unknown length
 14510 15861: contig of 1332 bp in length
 15862 15881: gap of unknown length
 15882 15921: contig of 1040 bp in length
 15922 15941: gap of unknown length
 15942 18485: contig of 1524 bp in length
 18486 18486: gap of unknown length
 18487 19316: contig of 831 bp in length
 19317 19337: gap of unknown length
 19337 20903: contig of 1567 bp in length
 20904 20923: gap of unknown length
 20924 22150: contig of 1227 bp in length
 22151 22170: gap of unknown length
 22171 23295: contig of 1135 bp in length
 23296 23315: gap of unknown length
 23316 24310: contig of 995 bp in length
 24311 24330: gap of unknown length
 24331 26217: contig of 1887 bp in length
 26218 26237: gap of unknown length
 26238 27815: gap of unknown length
 27816 27835: contig of 1578 bp in length
 27836 28794: gap of unknown length
 28795 28814: contig of 959 bp in length
 28815 30095: contig of 1281 bp in length
 30096 30115: gap of unknown length
 30116 31085: contig of 970 bp in length
 31086 31105: gap of unknown length
 31106 32390: contig of 1285 bp in length
 32391 32410: gap of unknown length
 32411 34245: contig of 1835 bp in length
 34246 34265: gap of unknown length
 34266 35631: contig of 1366 bp in length
 35632 35651: gap of unknown length
 35652 37059: contig of 1408 bp in length
 37060 37079: gap of unknown length
 37080 38607: contig of 1528 bp in length
 38608 38627: gap of unknown length
 38628 40420: contig of 1793 bp in length
 40421 40440: gap of unknown length
 40441 41701: contig of 1261 bp in length
 41702 41721: gap of unknown length
 41722 43319: contig of 1598 bp in length
 43320 43339: gap of unknown length
 43340 45717: contig of 2378 bp in length
 45718 45737: gap of unknown length
 45738 47273: contig of 1536 bp in length
 47274 47293: gap of unknown length
 47294 48892: contig of 1599 bp in length
 48893 48912: gap of unknown length
 48913 50344: contig of 1432 bp in length
 50345 50364: gap of unknown length
 50365 52143: contig of 1779 bp in length

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* 52144 52163: gap of unknown length
* 52164 54492: contig of 2329 bp in length
* 54493 54512: gap of unknown length
* 54513 56276: contig of 1764 bp in length
* 56277 56296: gap of unknown length
* 56297 57664: contig of 1368 bp in length
* 57665 57684: gap of unknown length
* 57685 59691: contig of 2007 bp in length
* 59692 59711: gap of unknown length
* 59712 63581: contig of 3870 bp in length
* 63582 63601: gap of unknown length
* 63602 65422: contig of 1821 bp in length
* 65423 65442: gap of unknown length
* 65443 67456: contig of 2014 bp in length
* 67457 67476: gap of unknown length
* 67477 69545: contig of 2069 bp in length
* 69546 69565: gap of unknown length
* 69566 72562: contig of 2997 bp in length
* 72563 72582: gap of unknown length
* 72583 75310: contig of 2728 bp in length
* 75311 75330: gap of unknown length
* 75331 77972: contig of 2642 bp in length
* 77973 77992: gap of unknown length
* 77993 82474: contig of 4482 bp in length
* 82475 82494: gap of unknown length
* 82495 85875: contig of 3381 bp in length.

FEATURES
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                /organism="Drosophila melanogaster"
                /db_xref="taxon:7227"
                /clone="RP11-19E11"

BASE COUNT   23385 a 18706 c 18751 g 23920 t 1113 others
ORIGIN
Query Match      1.3%: Score 21; DB 2; Length 85875;
Best Local Similarity 100.0%; Pred. No. 6; 2;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 262 attcgcgcgttgagagccac 282
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Db 37850 ACTCGCGCGGTGAGAGCCAC 37870

RESULT 12
AC012665/c 126039 bp DNA PRI 03-JUL-2001
LOCUS      Homo sapiens clone RP11-19E11, complete sequence.
DEFINITION
AC012665
AC012665.8 GI:14589661
KEYWORDS   HTG.
SOURCE      human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
            1 (bases 1 to 126039)
            Waterston, R.H.
            The sequence of Homo sapiens clone
            unpublished
            2 (bases 1 to 126039)
            Waterston, R.H.
            Direct Submission
            Submitted (02-NOV-1999) Genome Sequencing Center, Washington
            University School of Medicine, 4444 Forest Park Parkway, St. Louis,
            MO 63108, USA
            3 (bases 1 to 126039)
            Waterston, R.H.
            Direct Submission
            Submitted (03-JUL-2001) Genome Sequencing Center, Washington
            University School of Medicine, 4444 Forest Park Parkway, St. Louis,
            MO 63108, USA
            On Jul 3, 2001 this sequence version replaced gi:13794251.

REFERENCE
  AUTHORS   Waterston, R.H.
  TITLE     Direct Submission
  JOURNAL   Submitted (03-JUL-2001) Genome Sequencing Center, Washington
            University School of Medicine, 4444 Forest Park Parkway, St. Louis,
            MO 63108, USA
  COMMENT   On Jul 3, 2001 this sequence version replaced gi:13794251.

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----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUSGC
Web site: http://genome.wustl.edu/gsc/index.shtml
Project Information
Center project name: H.NH0019E11
-----

FEATURES
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                /db_xref="taxon:9606"
                /clone="RP11-19E11"

BASE COUNT   33691 a 29032 c 28371 g 34945 t
ORIGIN
Query Match      1.3%: Score 21; DB 9; Length 126039;
Best Local Similarity 100.0%; Pred. No. 6;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1537 cctggatcagctgcaaacaa 1557
      |||
Db 115904 CCTGGATCAGCTGCAAAACAA 115884

RESULT 13
AC084093/c 137569 bp DNA HTG 09-MAY-2001
LOCUS      Homo sapiens chromosome 8 clone CTD-2277K12 map 8, WORKING DRAFT
DEFINITION
AC084093
AC084093.2 GI:13123904
VERSION    HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
KEYWORDS   human.
SOURCE      Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
            1 (bases 1 to 137569)
            Birren, B., Linton, L., Nusbaum, C. and Lander, E.
            Homo sapiens chromosome 8, clone CTD-2277K12
            unpublished
            2 (bases 1 to 137569)
            Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N.,
            Anderson, S., Barna, N., Bastien, V., Bedalov, F., Boguski, L.,
            Bouckgalter, B., Brown, A., Burkett, G., Campiano, A., Castle, A.,
            Choapel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P.,
            DeRellano, K., Dewar, K., Diaz, J.S., Dodge, S., Ferreira, P.,
            Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S., Glade, S., Goyette, M.,
            Graham, L., Grand-Pierre, N., Hagos, B., Heaford, A., Horton, L.,
            Iliev, I., Johnson, R., Jones, C., Kann, L., Karatas, A., Larocque, K.,
            Lamazares, R., Landers, T., Lehoczy, J., Levine, R., Liu, C., Liu, G.,
            Macdonald, P., Margulis, N., McCarthy, M., McEwan, P., McKernan, K.,
            McPeckers, R., Meldrum, J., Meneus, L., Mihova, T., Mlenga, V.,
            Morrow, J., Murphy, T., Naylor, J., Norman, C.H., O'Connor, T.,
            O'Donnell, P., O'Neill, D., Oliver, T.W., Oliver, J., Peterson, K.,
            Pierre, N., Pisanil, C., Pollara, V., Raymond, C., Riback, M., Riley, R.,
            Rougov, P., Rothman, D., Roy, A., Santos, R., Schauer, S., Severy, P.,
            Sougnuez, C., Spencer, B., Stange-Thomann, N., Stojanovic, N.,
            Strauss, N., Subramanian, A., Talamas, J., Testaye, S., Theodore, J.,
            Tirrell, A., Travers, M., Triggillo, J., Vassiliev, H., Viel, R., Vo, A.,
            Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J.,
            Zimmer, A. and Zody, M.
            Direct Submission
            Submitted (12-OCT-2000) Whitehead Institute/MIT Center for Genome
            Research, 320 Charles Street, Cambridge, MA 02141, USA
            On Feb 26, 2001 this sequence version replaced gi:10799458.
            All repeats were identified using RepeatMasker:
            Smit, A.F.A. & Green, P. (1996-1997)
            http://ftp.genome.washington.edu/RM/RepeatMasker.html
            ----- Genome Center -----
            Center: Whitehead Institute/ MIT Center for Genome Research
            Center code: WIBR
            Web site: http://www-seq.wi.mit.edu

```

Contact: sequence_submissions@genome.wi.mit.edu
 Project Information
 Center project name: L11391
 Center clone name: 2277_K12
 Summary Statistics
 Sequencing Vector: Plasmid; n/a; 100% of reads
 Chemistry: Dye-terminator Big Dye; 100% of reads
 Assembly program: Phrap; version 0.960731
 Consensus quality: 136529 bases at least Q40
 Consensus quality: 137130 bases at least Q30
 Consensus quality: 137294 bases at least Q20
 Insert size: 139000; agarose-fp
 Quality coverage: 7.8 in Q20 bases; agarose-fp
 Quality coverage: 7.9 in Q20 bases; sum-of-coverage

NOTE: This is a 'working draft' sequence. It currently consists of 3 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

1 37849: contig of 37849 bp in length
 * 37850 37949: gap of 100 bp
 * 37950 82422: contig of 44473 bp in length
 * 82423 82522: gap of 100 bp
 * 82523 137569: contig of 55047 bp in length.
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 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /chromosome="8"
 /map="8"
 /clone="C2D-2277K12"
 /clone.lib="C2D Human BAC"
 1. 37849
 /note="assembly-fragment"
 misc_feature 37950..82422
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 /note="assembly-fragment"
 BASE COUNT 42095 a 26887 c 26629 g 41757 t 201 others
 ORIGIN

Query Match 1.3%; Score 21; DB 2; Length 137569;
 Best Local Similarity 100.0%; Pred. No. 6;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 863 gctgacgcctgacgacac 883
 ||||||||||||||||
 Db 33227 GCTGACGCCGACGACAC 33207

RESULT 14
 AC022846
 LOCUS
 DEFINITION Homo sapiens chromosome 8 clone RP11-253N21 map 8, WORKING DRAFT
 AC022846
 AC022846.3 GI:13123397
 HTG: HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
 KEYWORDS
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 163027)
 AUTHORS Birren,B., Linton,L., Nusbaum,C. and Lander,E.
 TITLE Homo sapiens chromosome 8, clone RP11-253N21
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 163027)

AUTHORS
 Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N., Anderson,S., Baldwin,J., Barna,N., Beckerly,R., Beda,F., Boguslavsky,L., Bouknight,B., Brown,A., Burkett,G., Castle,A., Choehel,Y., Colangelo,M., Collins,S., Collymore,A., Cooke,P., Dearrallano,K., Dewar,K., Domino,M., Doyle,M., Fennell,J., Ferreira,P., Fitzhugh,W., Forrest,C., Gage,D., Galagan,J., Gardina,S., Grant,G., Hages,B., Heald,A., Horton,L., Howland,J.C., Johnson,R., Jones,C., Kain,L., Karatas,A., Klein,J., Lander,E., Lenock,J., Levine,R., Liu,C., Liu,G., Locke,K., MacDonald,P., Marquis,N., McEwan,P., McGuck,A., McKernan,K., McNetters,R., Meldrum,T., Menus,L., Morrow,J., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P., Oliver,T.M., Peterson,K., Pierre,N., Pisanl,C., Pollara,V., Raymond,C., Riley,R., Rotman,D., Roy,A., Santos,R., Severy,P., Spencer,B., Stange-Rhoman,N., Stojanovic,N., Subramanian,A., Talmes,J., Tesfaye,S., Theodore,J., Titrell,A., Vassiliou,H., Viel,R., Vo,A., Wu,X., Wyman,D., Ye,W.J., Zimmer,A. and Zody,W.

TITLE
 JOURNAL
 COMMENT
 Submitted (06-FEB-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
 On Feb 25, 2001 this sequence version replaced g1:7139770.
 All repeats were identified using RepeatMasker:
 Smit, A.F.A. & Green, P. (1996-1997)
 http://ftp.genome.washington.edu/RM/RepeatMasker.html

Genome Center
 Center: Whitehead Institute/ MIT Center for Genome Research
 Center code: WIBR
 Web site: http://www.seq.wi.mit.edu
 Contact: sequence_submissions@genome.wi.mit.edu

Project Information
 Center project name: L6163
 Center clone name: 253.N.21

Summary Statistics
 Sequencing vector: M13; M7815; 3% of reads
 Sequencing vector: Plasmid; n/a; 61% of reads
 Chemistry: Dye-terminator Big Dye; 100% of reads
 Assembly program: Phrap; version 0.960731
 Consensus quality: 160669 bases at least Q40
 Consensus quality: 161671 bases at least Q30
 Consensus quality: 162136 bases at least Q20
 Insert size: 157000; agarose-fp
 Insert size: 162527; sum-of-coverage
 Quality coverage: 13.6 in Q20 bases; agarose-fp
 Quality coverage: 13.1 in Q20.

NOTE: This is a 'working draft' sequence. It currently consists of 6 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

1 23967: contig of 23967 bp in length
 * 23968 24067: gap of 100 bp
 * 24068 25128: contig of 1061 bp in length
 * 25129 25228: gap of 100 bp
 * 25229 34037: contig of 8809 bp in length
 * 34038 34137: gap of 100 bp
 * 34138 56813: contig of 22676 bp in length
 * 56814 56913: gap of 100 bp
 * 56914 92224: contig of 35311 bp in length
 * 92225 92324: gap of 100 bp
 * 92325 163027: contig of 70703 bp in length.
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 /db_xref="taxon:9606"
 /chromosome="8"
 /map="8"
 /clone="RP11-253N21"
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 1. 23967
 /note="assembly-fragment"

misc_feature


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repeat_region 11272. .11629
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repeat_region 12011. .12316
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repeat_region 12389. .12763
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repeat_region 12799. .13097
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repeat_region 13098. .13493
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repeat_region 13494. .13832
/rpt_family="MaLR"
repeat_region 13833. .14250
/rpt_family="ERV1"
repeat_region 14251. .15502
/rpt_family="MaLR"
repeat_region 15505. .15912
/rpt_family="MaLR"
repeat_region 15968. .16092
/rpt_family="ERV1"
repeat_region 16797. .17059
/rpt_family="MERL_type"
repeat_region 18122. .18307
/rpt_family="MERL_type"
repeat_region 18309. .18885
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/rpt_family="Alu"
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repeat_region 20844. .20938
/rpt_family="MIR"
repeat_region 20888. .21202
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repeat_region 21545. .21643
/rpt_family="L2"
repeat_region 21625. .21968
/rpt_family="L2"
repeat_region 22407. .22662
/rpt_family="ERV1"
repeat_region 22689. .22871
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repeat_region 23543. .23662
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repeat_region 23663. .23833
/rpt_family="MIR"
repeat_region 24159. .24465
/rpt_family="Alu"
repeat_region 24509. .24802
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/note="similar to EST BF589995 (NTD:911682319)"
misc_feature 24684. .25493
/note="CpG_Island (GC=73.5, o/e=0.80, #CpGs=89)"
misc_feature 25098. .25228
/note="similar to EST BF532525 (NTD:911619888)"
misc_feature 25180. .25228
/note="similar to EST BF787117 (NTD:912092153)"
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repeat_region 26345. .26419
/rpt_family="L2"
repeat_region 27624. .27751
/rpt_family="MIR"
Query Match 1.3%; Score 21; DB 9; Length 174822;
Best Local Similarity 100.0%; Pred. No. 5.8;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1537 cctgacacagtcgcaaaaca 1557
|||||
DB 6112 CCTGATCAGCTGCAAAACA 6132

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Search completed: February 15, 2002, 10:47:55
Job time: 2984 sec